

GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run On: March 13, 2003, 13:29:58 ; Search time 2 Seconds
(without alignments)
3.694 Million cell updates/sec

Title: us-09-837-602-1
Perfect score: 4403
Sequence: 1 ttggcagcagcgcggttg.....accgcggtggagctccagct 4403

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 839 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 2 summaries

Database : aa:*
1: /home/sdavid/sdavid-tmp/mar03/yu602/aa577530.gb_est1.*
2: /home/sdavid/sdavid-tmp/mar03/yu602/aa535711.gb_est1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	429.4	9.8	431	1	AA577530
2	408	9.3	408	2	AA535711

ALIGNMENTS

RESULT 1
AA577530
LOCUS
DEFINITION
n14b12.s1 NCI_CGAP_Col2 Homo sapiens cDNA clone IMAGE:1083839 3',
EST 03-SEP-1997
ACCESSION
AA577530
VERSION
AA577530.1 GI:2355004
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 431)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center

RESULT 2
AA535711/c
LOCUS
DEFINITION
nf88d08.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:926991 3',
EST 21-AUG-1997
ACCESSION
AA535711
VERSION
AA535711.1 GI:2279964
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbbrp/image/image.html
Seq primer: -40ml3 fwd. Et from Amersham
High quality sequence stop: 386.

FEATURES
Source

Location/Qualifiers
1. 431
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1083839"
/clone_lib="NCI_CGAP_Col2"
/sex="mixed"
/tissue_type="colon tumor"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: colon; Vector: Bluescript SK-; Site: 1: EcoRI
; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. Pooled colon tumors. 5' adaptor sequence: 5'
GAATTCGGCAGCGAG 3' 3' adaptor sequence: 5'
CTCGAGCTTTTCTTTTCTTTT 3' Average insert size: 1.2 kb."
BASE COUNT 178 a 68 c 85 g 100 t

Query Match 9.8%; Score 429.4; DB 1; Length 431;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 430; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1764 AACGAGATTAGAAATTCATGCTGAAAGTTCAAAACACAGGAGGAGATGTCATGTAGAA 1823
Db 1 AACGAGATTAGAAATTCATGCTGAAAGTTCAAAACACAGGAGGAGATGTCATGTAGAA 60

QY 1824 AAAGCCCAAGGATGATATAGACAAATGACACATTTTCAGTGTATGATGAGCAGTACCAAGAA 1883
Db 61 AAAGCCCAAGGATGATATAGACAAATGACACATTTTCAGTGTATGATGAGCAGTACCAAGAA 120

QY 1884 GTACCAAAATATCTCAAGAAAATGAAATTTGGGAAGAAAGTGAACCTCAAGGAAGAGATCAC 1943
Db 121 GTACCAAAATATCTCAAGAAAATGAAATTTGGGAAGAAAGTGAACCTCAAGGAAGAGATCAC 180

QY 1944 TATGTCAGCTAAAGAAATATCTAACAATGACAACTTCAGGATGATGAGTGTCTTC 2003
Db 181 TATGTCAGCTAAAGAAATATCTAACAATGACAACTTCAGGATGATGAGTGTCTTC 240

QY 2004 CAAAAAGCTGTATTGACTGATGATTTAGTCACTGGTGTATTAATAAATCTACTTCCAGAA 2063
Db 241 CAAAAAGCTGTATTGACTGATGATTTAGTCACTGGTGTATTAATAAATCTACTTCCAGAA 300

QY 2064 ATCCCTCTGGCAATAATGATGATTTGTCACACTAAAAATTTCAAGAAATTCAAAAAGG 2123
Db 301 ATCCCTCTGGCAATAATGATGATTTGTCACACTAAAAATTTCAAGAAATTCAAAAAGG 360

QY 2124 TCACATATCTCTGGAGCAGAGAAACCTTCACACATCATTTGGAGGATCAGATCTAATAGCTC 2183
Db 361 TCACATATCTCTGGAGCAGAGAAACCTTCACACATCATTTGGAGGATCAGATCTAATAGCTC 420

QY 2184 ATCATGCTCGA 2194
Db 421 ATCATGCTCGA 431

RESULT 2
AA535711/c
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